What is claimed is:

1. A method of diagnosing susceptibility to schizophrenia in a patient, the method comprising: determining the presence or absence of an allele of a polymorphic marker in the DNA of the patient, wherein the polymorphic marker is within a segment of chromosome 1q22 bordered by D1S2705 and D1S1679 and is linked to a DNA segment (SCZ) having a variant form associated with a phenotype of schizophrenia, and said allele is in phase with the variant form of SCZ, whereby the presence of said allele in the patient indicates susceptibility to schizophrenia.

2. The method of claim 1, wherein the polymorphic marker is APOA2, FcER1G, FcGR2A, B426K24T, or D1S2675.

3. The method of claim 1, wherein the polymorphic marker is within 4 cM of the B426K24T marker.

4. The method of claim 1, wherein the polymorphic marker is between B426K24T and D1S2675.

5. The method of claim 1, wherein the allele is in linkage disequilibrium with the DNA segment.

6. The method of claim 1, further comprising the step of establishing that the allele is in phase with the variant form of the DNA segment.

7. The method of claim 6, wherein the establishing step comprises determining the presence or absence of the allele in first and second degree relatives of the patient, the first and second degree relative each being of known phenotype for schizophrenia, at least one of

the relatives having a phenotype of schizophrenia and being informative for the allele.

8. The method of claim 7, further comprising the step of determining the phenotypes of relatives.

9. The method of claim 8, wherein the phenotypes of the relatives are determined by the DSM-IIIR criteria of Table 1 and Table 2.

10. The method of claim 9, wherein one of the relatives is a parent or sibling of the patient.

11. The method of claim 1, further comprising the step of determining the presence or absence of an allele of a second polymorphic marker in the patient.

12. The method of claim 1, wherein the presence or absence of the allele is determined by amplifying a segment of DNA within chromosome 1q22 that spans the polymorphic marker.

13. The method of claim 12, further comprising the step of determining the size of the amplified segment.

14. The method of claim 12, further comprising the step of determining the sequence of the amplified segment.

15. The method of claim 12, further comprising the step of determining the presence or absence of a restriction enzyme site within the amplified segment.

16. The method of claim 1, wherein the presence or absence of the allele is determined by contacting the

DNA from the patient with an oligonucleotide probe capable of hybridizing to the allele under stringent conditions; and determining whether hybridization has occurred thereby indicating the presence of the allele.

17. The method of claim 16, further comprising the step of isolating a sample of DNA from the patient.

18. The method of claim 17, wherein the DNA is genomic and the sample is obtained from saliva, blood or buccal mucosal cells.

19. A method for determining the presence of an alteration in the SCZ promoter sequence, said alteration being associated with a schizophrenic condition, said method comprising:

a) providing a nucleic acid molecule comprising a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO: 3, and SEQ ID NO:4;

b) isolating the corresponding sequence from a test subject suspected of having an alteration in the SCZ promoter;

c) forming a heteroduplex between the sequence of step a) and step b); and

d) assessing said duplex for the presence of an alteration selected from the group consisting of a mismatch, an insertion and a deletion.

20. A method for assessing a test compound for SCZ protein modulating activity, comprising:

a) providing a purified SCZ protein selected from the group of sequences having SEQ ID NO: 2 or SEQ ID NO: 5;

b) contacting said SCZ protein with an agent suspected on modulating SCZ protein activity;